



PCT

RAW SEQUENCE LISTING

DATE: 09/09/2004

PATENT APPLICATION: US/10/506,406

TIME: 15:58:04

Input Set : D:\9471-011-999.TXT

Output Set: N:\CRF4\09092004\J506406.raw

4 <110> APPLICANT: Swiercz, Rafal
 5 Selman, Steven
 6 Jankun, Jerzy
 7 Chorostowska-Wynimko, Joanna
 8 Skrzypczak-Jankun, Ewa
 10 <120> TITLE OF INVENTION: MODIFIED PLASMINOGEN ACTIVATOR INHIBITOR
 11 TYPE-1 AND METHODS BASED THEREON
 14 <130> FILE REFERENCE: 9471-011-999
 C--> 16 <140> CURRENT APPLICATION NUMBER: US/10/506,406
 C--> 17 <141> CURRENT FILING DATE: 2004-09-01
 19 <150> PRIOR APPLICATION NUMBER: PCT/US03/06679
 20 <151> PRIOR FILING DATE: 2003-03-04
 22 <150> PRIOR APPLICATION NUMBER: 60/361,670
 23 <151> PRIOR FILING DATE: 2002-03-04
 25 <160> NUMBER OF SEQ ID NOS: 3
 27 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 2876
 31 <212> TYPE: DNA
 32 <213> ORGANISM: Homo sapiens
 34 <220> FEATURE:
 35 <221> NAME/KEY: CDS
 36 <222> LOCATION: (76)...(1281)
 37 <223> OTHER INFORMATION: human PAI-1 plus 5' and 3' sequence
 39 <400> SEQUENCE: 1
 40 gaattcctgc agctcagcag ccgcccgcag agcaggacga accgccaatc gcaaggcacc 60
 41 tctgagaact tcagg atg cag atg tct cca gcc ctc acc tgc cta gtc ctg 111
 42 Met Gln Met Ser Pro Ala Leu Thr Cys Leu Val Leu
 43 1 5 10
 45 ggc ctg gcc ctt gtc ttt ggt gaa ggg tct gct gtg cac cat ccc cca 159
 46 Gly Leu Ala Leu Val Phe Gly Glu Gly Ser Ala Val His His Pro Pro
 47 15 20 25
 49 tcc tac gtg gcc cac ctg gcc tca gac ttc ggg gtg agg gtg ttt cag 207
 50 Ser Tyr Val Ala His Leu Ala Ser Asp Phe Gly Val Arg Val Phe Gln
 51 30 35 40
 53 cag gtg gcg cag gcc tcc aag gac cgc aac gtg gtt ttc tca ccc tat 255
 54 Gln Val Ala Gln Ala Ser Lys Asp Arg Asn Val Val Phe Ser Pro Tyr
 55 45 50 55 60
 57 ggg gtg gcc tcg gtg ttg gcc atg ctc cag ctg aca aca gga gga gaa 303
 58 Gly Val Ala Ser Val Leu Ala Met Leu Gln Leu Thr Thr Gly Gly Glu
 59 65 70 75
 61 acc cag cag cag att caa gca gct atg gga ttc aag att gat gac aag 351
 62 Thr Gln Gln Gln Ile Gln Ala Ala Met Gly Phe Lys Ile Asp Asp Lys

Does Not Comply
Corrected Diskette Needed

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63		80		85		90		
65	ggc atg gcc ccc gcc ctc cgg cat ctg tac aag gag ctc atg ggg cca	399						
66	Gly Met. Ala Pro Ala Leu Arg His Leu Tyr Lys Glu Leu Met Gly Pro							
67		95		100		105		
69	tgg aac aag gat gag atc agc acc aca gac gcg atc ttc gtc cag cgg	447						
70	Trp Asn Lys Asp Glu Ile Ser Thr Thr Asp Ala Ile Phe Val Gln Arg							
71		110		115		120		
73	gat ctg aag ctg gtc cag ggc ttc atg ccc cac ttc ttc agg ctg ttc	495						
74	Asp Leu Lys Leu Val Gln Gly Phe Met Pro His Phe Phe Arg Leu Phe							
75	125		130		135		140	
77	cgg agc acg gtc aag caa gtg gac ttt tca gag gtg gag aga gcc aga	543						
78	Arg Ser Thr Val Lys Gln Val Asp Phe Ser Glu Val Glu Arg Ala Arg							
79		145		150		155		
81	ttc atc atc aat gac tgg gtg aag aca cac aca aaa ggt atg atc agc	591						
82	Phe Ile Ile Asn Asp Trp Val Lys Thr His Thr Lys Gly Met Ile Ser							
83		160		165		170		
85	aac ttg ctt ggg aaa gga gcc gtg gac cag ctg aca cgg ctg gtg ctg	639						
86	Asn Leu Leu Gly Lys Gly Ala Val Asp Gln Leu Thr Arg Leu Val Leu							
87		175		180		185		
89	gtg aat gcc ctc tac ttc aac ggc cag tgg aag act ccc ttc ccc gac	687						
90	Val Asn Ala Leu Tyr Phe Asn Gly Gln Trp Lys Thr Pro Phe Pro Asp							
91		190		195		200		
93	tcc agc acc cac cgc cgc ctc ttc cac aaa tca gac ggc agc act gtc	735						
94	Ser Ser Thr His Arg Arg Leu Phe His Lys Ser Asp Gly Ser Thr Val							
95	205		210		215		220	
97	tct gtg ccc atg atg gct cag acc aac aag ttc aac tat act gag ttc	783						
98	Ser Val Pro Met Met Ala Gln Thr Asn Lys Phe Asn Tyr Thr Glu Phe							
99		225		230		235		
101	acc acg ccc gat ggc cat tac tac gac atc ctg gaa ctg ccc tac cac	831						
102	Thr Thr Pro Asp Gly His Tyr Tyr Asp Ile Leu Glu Leu Pro Tyr His							
103		240		245		250		
105	ggg gac acc ctc agc atg ttc att gct gcc cct tat gaa aaa gag gtg	879						
106	Gly Asp Thr Leu Ser Met Phe Ile Ala Ala Pro Tyr Glu Lys Glu Val							
107		255		260		265		
109	cct ctc tct gcc ctc acc aac att ctg agt gcc cag ctc atc agc cac	927						
110	Pro Leu Ser Ala Leu Thr Asn Ile Leu Ser Ala Gln Leu Ile Ser His							
111		270		275		280		
113	tgg aaa ggc aac atg acc agg ctg ccc cgc ctc ctg gtt ctg ccc aag	975						
114	Trp Lys Gly Asn Met Thr Arg Leu Pro Arg Leu Leu Val Leu Pro Lys							
115	285		290		295		300	
117	ttc tcc ctg gag act gaa gtc gac ctc agg aag ccc cta gag aac ctg	1023						
118	Phe Ser Leu Glu Thr Glu Val Asp Leu Arg Lys Pro Leu Glu Asn Leu							
119		305		310		315		
121	gga atg acc gac atg ttc aga cag ttt cag gct gac ttc acg agt ctt	1071						
122	Gly Met Thr Asp Met Phe Arg Gln Phe Gln Ala Asp Phe Thr Ser Leu							
123		320		325		330		
125	tca gac caa gag cct ctc cac gtc gcg cag gcg ctg cag aaa gtg aag	1119						
126	Ser Asp Gln Glu Pro Leu His Val Ala Gln Ala Leu Gln Lys Val Lys							
127		335		340		345		

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129 atc gag gtg aac gag agt ggc acg gtg gcc tcc tca tcc aca gct gtc 1167
130 Ile Glu Val Asn Glu Ser Gly Thr Val Ala Ser Ser Ser Thr Ala Val
131 350 355 360
133 ata gtc tca gcc cgc atg gcc ccc gag gag atc atc atg gac aga ccc 1215
134 Ile Val Ser Ala Arg Met Ala Pro Glu Glu Ile Ile Met Asp Arg Pro
135 365 370 375 380
137 ttc ctc ttt gtg gtc cgg cac aac ccc aca gga aca gtc ctt ttc atg 1263
138 Phe Leu Phe Val Val Arg His Asn Pro Thr Gly Thr Val Leu Phe Met
139 385 390 395
141 ggc caa gtg atg gaa ccc tgaccctggg gaaagacgcc ttcactctggg 1311
142 Gly Gln Val Met Glu Pro
143 400
145 acaaaactgg agatgcatcg ggaaagaaga aactccgaag aaaagaattt tagtggttaat 1371
146 gactctttct gaaggaagag aagacatttg ccttttgtaa aaagatggta aaccagatct 1431
147 gtctccaaga ccttggcctc tccttgaggg accttttaggt caaactccct agtctccacc 1491
148 tgagaccctg ggagagaagt ttgaagcaca actcccttaa ggtctccaaa ccagacgggtg 1551
149 acgcctgcgg gaccatctgg ggcacctgct tccaccgcgc tctctgceca ctggggtctg 1611
150 cagacctggg tccactgag gccctttgca ggatggaact acggggctta caggagcttt 1671
151 tgtgtgcctg gtagaaacta tttctgttcc agtcacattg ccatcactct tgtactgcct 1731
152 gccaccgcgg aggaggctgg tgacaggcca aaggccagtg gaagaaacac cctttcatct 1791
153 cagagtccac tgtggcactg gccaccctc cccagtacag ggggtgctgca ggtggcagag 1851
154 tgaatgtccc ccatcatgtg gcccactct cctggcctgg ccatctccct cccagaaac 1911
155 agtgtgcatg gggtattttg gagtgtaggt gacttgttta ctcatgaag cagatttctg 1971
156 cttcctttta ttttatagg aatagaggaa gaaatgtcag atgctgccc agctcttcac 2031
157 cccccaatct cttgggtggg aggggtgtac ctaaataatt atcatatcct tgcccttgag 2091
158 tgcttgtag agagaaagag aactactaag gaaaataata ttatttaaac tcgctcctag 2151
159 tgtttctttg tgggtctgtg caccgtatct caggaagtcc agccacttga ctggcacaca 2211
160 cccctccgga catccagcgt gacggagccc aactgccac cttgtggcgg cctgagaccc 2271
161 tcgcgcccc cgcgcccccc gcgcccctct ttttcccctt gatggaaatt gaccatacaa 2331
162 tttcatcctc cttcagggga tcaaaaggac ggagtggggg gacagagact cagatgagga 2391
163 cagagtgggt tccaatgtgt tcaatagatt taggagcaga aatgcaaggg gctgcatgac 2451
164 ctaccaggac agaactttcc ccaattacag ggtgactcac agccgcattg gtgactcact 2511
165 tcaatgtgtc atttccggct gctgtgtgtg agcagtggac acgtgagggg ggggtgggtg 2571
166 agagagacag gcagctcgga ttcaactacc ttagataata tttctgaaaa cctaccagcc 2631
167 agagggtagg gcacaaagat ggatgtaatg cactttggga ggccaaggcg ggaggattgc 2691
168 ttgagcccag gagttcaaga ccagcctggg caacatacca agaccccgt ctctttaaaa 2751
169 atatatatat tttaaatata cttaaataata tatttctaata atctttaaat atatatatat 2811
170 attttaaaga ccaatttatg ggagaattgc acacagatgt gaaatgaatg taatctaata 2871
171 gaagc 2876
173 <210> SEQ ID NO: 2
174 <211> LENGTH: 402
175 <212> TYPE: PRT 0
176 <213> ORGANISM: Homo sapiens
178 <220> FEATURE:
179 <223> OTHER INFORMATION: human PAI-1 amino acid sequence, including signal peptide
181 <400> SEQUENCE: 2
182 Met Gln Met Ser Pro Ala Leu Thr Cys Leu Val Leu Gly Leu Ala Leu
183 1 5 10 15
184 Val Phe Gly Glu Gly Ser Ala Val His His Pro Pro Ser Tyr Val Ala

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185          20          25          30
186 His Leu Ala Ser Asp Phe Gly Val Arg Val Phe Gln Gln Val Ala Gln
187          35          40          45
188 Ala Ser Lys Asp Arg Asn Val Val Phe Ser Pro Tyr Gly Val Ala Ser
189          50          55          60
190 Val Leu Ala Met Leu Gln Leu Thr Thr Gly Gly Glu Thr Gln Gln Gln
191 65          70          75          80
192 Ile Gln Ala Ala Met Gly Phe Lys Ile Asp Asp Lys Gly Met Ala Pro
193          85          90          95
194 Ala Leu Arg His Leu Tyr Lys Glu Leu Met Gly Pro Trp Asn Lys Asp
195          100          105          110
196 Glu Ile Ser Thr Thr Asp Ala Ile Phe Val Gln Arg Asp Leu Lys Leu
197          115          120          125
198 Val Gln Gly Phe Met Pro His Phe Phe Arg Leu Phe Arg Ser Thr Val
199          130          135          140
200 Lys Gln Val Asp Phe Ser Glu Val Glu Arg Ala Arg Phe Ile Ile Asn
201 145          150          155          160
202 Asp Trp Val Lys Thr His Thr Lys Gly Met Ile Ser Asn Leu Leu Gly
203          165          170          175
204 Lys Gly Ala Val Asp Gln Leu Thr Arg Leu Val Leu Val Asn Ala Leu
205          180          185          190
206 Tyr Phe Asn Gly Gln Trp Lys Thr Pro Phe Pro Asp Ser Ser Thr His
207          195          200          205
208 Arg Arg Leu Phe His Lys Ser Asp Gly Ser Thr Val Ser Val Pro Met
209          210          215          220
210 Met Ala Gln Thr Asn Lys Phe Asn Tyr Thr Glu Phe Thr Thr Pro Asp
211 225          230          235          240
212 Gly His Tyr Tyr Asp Ile Leu Glu Leu Pro Tyr His Gly Asp Thr Leu
213          245          250          255
214 Ser Met Phe Ile Ala Ala Pro Tyr Glu Lys Glu Val Pro Leu Ser Ala
215          260          265          270
216 Leu Thr Asn Ile Leu Ser Ala Gln Leu Ile Ser His Trp Lys Gly Asn
217          275          280          285
218 Met Thr Arg Leu Pro Arg Leu Leu Val Leu Pro Lys Phe Ser Leu Glu
219          290          295          300
220 Thr Glu Val Asp Leu Arg Lys Pro Leu Glu Asn Leu Gly Met Thr Asp
221 305          310          315          320
222 Met Phe Arg Gln Phe Gln Ala Asp Phe Thr Ser Leu Ser Asp Gln Glu
223          325          330          335
224 Pro Leu His Val Ala Gln Ala Leu Gln Lys Val Lys Ile Glu Val Asn
225          340          345          350
226 Glu Ser Gly Thr Val Ala Ser Ser Ser Thr Ala Val Ile Val Ser Ala
227          355          360          365
228 Arg Met Ala Pro Glu Glu Ile Ile Met Asp Arg Pro Phe Leu Phe Val
229          370          375          380
230 Val Arg His Asn Pro Thr Gly Thr Val Leu Phe Met Gly Gln Val Met
231 385          390          395          400
232 Glu Pro
235 <210> SEQ ID NO: 3

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Output Set: N:\CRF4\09092004\J506406.raw

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236 <211> LENGTH: 379
237 <212> TYPE: PRT
238 <213> ORGANISM: Homo sapiens
240 <220> FEATURE:
241 <223> OTHER INFORMATION: human PAI-1 mature amino acid sequence
243 <400> SEQUENCE: 3
244 Val His His Pro Pro Ser Tyr Val Ala His Leu Ala Ser Asp Phe Gly
245 1 5 10 15
246 Val Arg Val Phe Gln Gln Val Ala Gln Ala Ser Lys Asp Arg Asn Val
247 20 25 30
248 Val Phe Ser Pro Tyr Gly Val Ala Ser Val Leu Ala Met Leu Gln Leu
249 35 40 45
250 Thr Thr Gly Gly Glu Thr Gln Gln Gln Ile Gln Ala Ala Met Gly Phe
251 50 55 60
252 Lys Ile Asp Asp Lys Gly Met Ala Pro Ala Leu Arg His Leu Tyr Lys
253 65 70 75 80
254 Glu Leu Met Gly Pro Trp Asn Lys Asp Glu Ile Ser Thr Thr Asp Ala
255 85 90 95
256 Ile Phe Val Gln Arg Asp Leu Lys Leu Val Gln Gly Phe Met Pro His
257 100 105 110
258 Phe Phe Arg Leu Phe Arg Ser Thr Val Lys Gln Val Asp Phe Ser Glu
259 115 120 125
260 Val Glu Arg Ala Arg Phe Ile Ile Asn Asp Trp Val Lys Thr His Thr
261 130 135 140
262 Lys Gly Met Ile Ser Asn Leu Leu Gly Lys Gly Ala Val Asp Gln Leu
263 145 150 155 160
264 Thr Arg Leu Val Leu Val Asn Ala Leu Tyr Phe Asn Gly Gln Trp Lys
265 165 170 175
266 Thr Pro Phe Pro Asp Ser Ser Thr His Arg Arg Leu Phe His Lys Ser
267 180 185 190
268 Asp Gly Ser Thr Val Ser Val Pro Met Met Ala Gln Thr Asn Lys Phe
269 195 200 205
270 Asn Tyr Thr Glu Phe Thr Thr Pro Asp Gly His Tyr Tyr Asp Ile Leu
271 210 215 220
272 Glu Leu Pro Tyr His Gly Asp Thr Leu Ser Met Phe Ile Ala Ala Pro
273 225 230 235 240
274 Tyr Glu Lys Glu Val Pro Leu Ser Ala Leu Thr Asn Ile Leu Ser Ala
275 245 250 255
276 Gln Leu Ile Ser His Trp Lys Gly Asn Met Thr Arg Leu Pro Arg Leu
277 260 265 270
278 Leu Val Leu Pro Lys Phe Ser Leu Glu Thr Glu Val Asp Leu Arg Lys
279 275 280 285
280 Pro Leu Glu Asn Leu Gly Met Thr Asp Met Phe Arg Gln Phe Gln Ala
281 290 295 300
282 Asp Phe Thr Ser Leu Ser Asp Gln Glu Pro Leu His Val Ala Gln Ala
283 305 310 315 320
284 Leu Gln Lys Val Lys Ile Glu Val Asn Glu Ser Gly Thr Val Ala Ser
285 325 330 335
286 Ser Ser Thr Ala Val Ile Val Ser Ala Arg Met Ala Pro Glu Glu Ile

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/506,406

DATE: 09/09/2004

TIME: 15:58:05

Input Set : D:\9471-011-999.TXT

Output Set: N:\CRF4\09092004\J506406.raw

L:16 M:270 C: Current Application Number differs, Replaced Current Application Number

L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date